

RESULT	2	
Q9SEW4		
ID	Q9SEW4	PRELIMINARY; PRT: 593 AA.
AC	Q9SEW4	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, last sequence update)	
DT	01-OCT-2000 (TREMBLrel. 15, last annotation update)	
DE	VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).	
OS	Juglans regia (English walnut).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;	
OC	Fagales; Juglandaceae; Juglans.	
OX	NCBI_TaxID=51240;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=CV. SONLAD; TISSUE=SONATIC EMBRYO LINE;	
RA	Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;	
RT	"Identification and cloning of a cDNA encoding a vicilin-like protein,	
RT	Jug r 2, from English walnut kernel (Juglans regia): a major food	
RT	allergen."	
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF066055; AAF18269.1; "	
DR	HSSP; P02853; 2PHL.	
DR	INTERPRO; IPR001113; "	
DR	PFAM; PF00546; Seedstore_7s; 1.	
FT	NON_TER	
SO	SEQUENCE	593 AA: 69990 MW: 99A127E19B18C0D8 CRC64:

Query Match	52.2%;	Score 117.5;	DB 10;	Length 593;
Best Local Similarity	46.3%;	Pred. No. 8.6e-07;		
Matches 19;	Conservative 14;	Mismatches 7;	Indels 1;	Gaps 1;

QY 1 PEDPQRRYEECCQQEC-RQGEERQQPQCQCRCLTKRFEEQQQ 40
| : : : : : | : : : : : | : : : : :
Db 69 PRDPEQRVECCQQCCERQRRGQEQLCKRRCEQRQRQGEERE 109

RESULT	3	
09SP15		
ID	09SP15	PRELIMINARY; PRT; 666 AA.
AC	09SP15;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last annotation update)	
DE	VICILIN PRECURSOR.	
GN	AMP2.	
OS	Macadamia integrifolia (Macadamia nut).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.	
OX	NCBI_TaxID=60698;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=NUT KERNEL;	
RA	Marcus J.P., Goulier K.C., Green J.L., Manners J.M.;	
RT	"A family of antimicrobial peptides is produced by processing of a 7S	
RT	globulin protein in Macadamia integrifolia kernels.";	
RL	Plant J. 0:0-0(1999).	
DR	EMBL; AF161883; AAD54244.1; -.	
DR	HSSP; P02853; 2PIL.	
DR	INTERPRO; IPR001113; -.	
DR	PFAM; PF00546; Seedstore_7s.1.	
SO	SEQUENCE	666 AA; 78217 MW; C752B884B2DF0224 CRC64;

Query Match	50.7%	Score 114	DB 10	Length 666
Best Local Similarity	47.5%	Pred. 1.25e-06		
Matches 19	Conservative 11	Mismatches 8	Indels 2	Gaps 1
3	DPORRYECCOEC--RQOEERQPPCCQCRCLKRFQEDQQ	40		
: :	:		: : : : :	

Db 121 DPOQYEOCCKHCQRRETEPHMOTCQQRCEKRYEKEKK 160

RESULT	4
Q9SP_L3	
ID	Q9SP_L3
AC	Q9SP_L3;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE	VICILIN PRECURSOR (FRAGMENT).
GN	AMP2.
OS	Macadamia integrifolia (Macadamia nut).
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
OX	NCBI_TaxId=60698;
RP	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=NUT KERNEL;
RT	Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT	"A family of antimicrobial peptides is produced by processing of a 7
RT	globulin protein in Macadamia integrifolia.";
RT	Plant J. 0-0-0(1999)
EMBL	EMBL; AF161885; AAD54246.1; -.
DR	HSSP; P02853; 2PHL.
DR	INTERPRO; IPR001113; -.
PFAM	PFAM; PF00546; Seedstore_7s; 1.
FT	NON_TER
SQ	SEQUENCE 625 AA; 73586 MW; 415808A89D370296 CRC64;

Query Match	49.8%;	Score 112;	DB 10;	Length 625;
Best Local Similarity	-47.5%;	Pred. NO. 4.2e-06;		
Matches 19; Conservative	11;	Mismatches 8;	Indels 2;	Gaps 1;

Qy 3 DPQRREECQQEC-ROEEERQPCCCRCLKFEQEEOO 40
| | | | | : | | | | | : | | | |
Db 80 DPQQQDEQCRCRCRRETEPRHHIQCGRCEREYEEKRK 115

RESULT	5	Q9SP14			
ID	Q9SP14	PRELIMINARY;	PRT;	666	AA.
AC	Q9SP14;				
DT	01-MAY-2000 (TREMBlrel. 13, Created)				
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)				
DT	01-OCT-2000 (TREMBlrel. 15, Last annotation update)				
DE	VITILIN PRECURSOR.				
GN	AMP2.				
OS	Macadamia integrifolia (Macadamia nut).				
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;				
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.				
OX	NCBI_TaxID=60698;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=NOT KNOWN;				
RA	Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;				
RT	"A family of antimicrobial peptides is produced by processing of a 75				
RT	globulin protein in Macadamia integrifolia.";				
RT	Plant J. 0:0-0(1999).				
DR	EMBL; AF161884; AAD54245.1;				
DR	HSSP; P02853; 2PIL.				
DR	INTERPRO; IPR001113;				
DR	PRAM; PF00546; Seedstore_7s; 1.				
SO	SEQUENCE	666	AA;	78243	MM; OECA22F8710F8A7B CRC64;

Query Match	49.8%	Score 112	DB 10	Length 666
Best Local Similarity	56.4%	Pred. No. 4,46-06		
Matches 22	Conservative	7	Mismatches 4	Indels 6
				Gaps 2
OY	3	DPORR-YEECCQEGCRQEEFRQDPCCQCGCLKRFEEDEQQ	40	

DT 01-MAY-2000 (TEMBLrel. 13, last sequence update)
DE TATA BOX-BINDING PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92350691; PubMed=1641350;
RA Hashimoto S., Fujita H., Hasegawa S., Roeder R.G., Horikoshi M.,
RT "Conserved structural motifs within the N-terminal domain of TFIID tau
from Xenopus, mouse and human."
RL Nucleic Acids Res. 20:3788-3788(1992).
SQ SEQUENCE 154 AA; 16790 MW; 93A5A0B5C6AFC604 CRC64;

Query Match 36.4%; Score 82; DB 4; Length 154;
Best Local Similarity 41.0%; Pred. No. 0.0057;
Matches 16; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

OY 2 EDPQRRYECQCEKROEERQCPQCCORCLKRFEEQEQ 40
|: ||:: ||: ||::|| ||: ||: ||: ||:
Db 53 EEOQRQOQOQOQOQOQOQOQOQOQOQOQOQOQ 91

RESULT 10

ID 016845 PRELIMINARY; PRT; 339 AA.

AC Q16845;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-JUN-1998 (TEMBLrel. 06, last sequence update)
DE 01-MAY-2000 (TEMBLrel. 13, last annotation update)
DE TRANSCRIPTION INITIATION FACTOR TFIID (TATA-BOX FACTOR) (TATA
DE SEQUENCE-BINDING PROTEIN) (TBP).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=FIBROBLAST;
RA Kao C., Lieberman P., Schmidt M., Zhou Q., Pei R., Berk A.J.;
RA Submitted (JUN-1990) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION
CC OF EUKARYOTIC GENES TRANSCRIBED BY RNA POLYMERASE II. TFIID BINDS
CC SPECIFICALLY TO THE TATA BOX PROMOTER ELEMENT WHICH LIES CLOSE TO
CC THE POSITION OF TRANSCRIPTION INITIATION.
CC -1- SUBUNIT: BINDS DNA AS A MONOMER.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: THE C-TERMINAL 180 RESIDUES ARE EXTREMELY WELL
CC CONSERVED IN ALL EUKARYOTIC TFIID
CC -1- SIMILARITY: WEAK, WITH BACTERIAL POLYMERASE SIGMA-FACTORS.
EMBL: M4960; AAC03409.1; -.
DR HSSP: P20226; ITGH.
DR INTERPRO: IPR000814; -.
DR PFAM: PF00352; TBP; 2.
DR PRINTS: PR00686; TIFACTORIID.
DR PROSITE: PS00351; TFIID; 2.
KW Transcription regulation; DNA-binding; Nuclear protein; Duplication.
SQ SEQUENCE 339 AA; 37783 MW; 98B7E26CB42B853A CRC64;

Query Match 36.4%; Score 82; DB 4; Length 339;
Best Local Similarity 41.0%; Pred. No. 0.011;
Matches 16; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

OY 2 EDPQRRYECQCEKROEERQCPQCCORCLKRFEEQEQ 40
|: ||:: ||: ||::|| ||: ||: ||: ||:
Db 53 EEOQRQOQOQOQOQOQOQOQOQOQOQOQOQOQ 91

RESULT 11

ID 090957 PRELIMINARY; PRT; 2123 AA.

AC Q90957;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, last annotation update)
DE ADENYLYL CYCLASE.
GN ACRA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Dictyostellida; Dictyostellium.
OX NCBI_TaxID=44689;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Soderbom F., Anjard C., Tranfar N., Loomis W.F.;
RT "An adenylyl cyclase that functions during late development of
RT Dictyostellium."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF153362; AAD50121.1; -.
DR HSSP: P19754; JAWK.
DR INTERPRO: IPR000410; -.
DR INTERPRO: IPR001054; -.
DR INTERPRO: IPR001440; -.
DR INTERPRO: IPR001596; -.
DR INTERPRO: IPR001789; -.
DR PFAM: PF00072; response_reg; 1.
DR PFAM: PF00211; guanylate_cyc; 1.
DR PRINTS: PR00344; BCTRSENSOR.
DR PROSITE: PS00387; PPASe; UNKNOWN_1.
SQ SEQUENCE 2123 AA; 243039 MW; 744247140BC342FA CRC64;

Query Match 36.2%; Score 81.5; DB 5; Length 2123;
Best Local Similarity 43.6%; Pred. No. 0.056;
Matches 17; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

OY 2 EDPQRRYECQCEKROEERQCPQCCORCLKRFEEQEQ 40
|: ||:: ||: ||::|| ||: ||: ||: ||:
Db 1932 QQQQRRQOQOQOQOQOQOQOQOQOQOQOQ 1969

RESULT 12

ID Q9W352 PRELIMINARY; PRT; 663 AA.

AC Q9W352;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, last sequence update)
DT 01-JUN-2000 (TEMBLrel. 14, last annotation update)
DE CG17446 PROTEIN.
GN CG17446.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Cealniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriil J.F., Agbayani A., An H.-J., Andrews-Plankkoch C., Baldwin D.,

